

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/618, 143A  
Source: TFW16  
Date Processed by STIC: 10/12/2006

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 10/12/2006

PATENT APPLICATION: US/10/618,143A

TIME: 15:56:29

Input Set : A:\078-us1.ST25.txt

Output Set: N:\CRF4\10122006\J618143A.raw

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3 <110> APPLICANT: Paz Einat, Louis Deiss, and Ruth Maya
5 <120> TITLE OF INVENTION: ISOCITRATE DEHYDROGENASE AND USES THEREOF
7 <130> FILE REFERENCE: 67723-A; 078-US1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/618,143A
C--> 10 <141> CURRENT FILING DATE: 2003-07-11
12 <150> PRIOR APPLICATION NUMBER: 60/395364
13 <151> PRIOR FILING DATE: 2002-07-11
15 <160> NUMBER OF SEQ ID NOS: 6
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2301
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (247)..(1491)
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34 tgtactttaa accggataaa ctgggctgtc tggcaggcga taaactacat tcagttgagt      180
36 ctgcaagact gggaggaact ggggtgataa gaaatctatt cactgtcaag gtttattgaa      240
38 gtcaaa atg tcc aaa aaa atc agt ggc ggt tct gtg gta gag atg caa      288
39 Met Ser Lys Lys Ile Ser Gly Gly Ser Val Val Glu Met Gln
40 1 5 10
42 gga gat gaa atg aca cga atc att tgg gaa ttg att aaa gag aaa ctc      336
43 Gly Asp Glu Met Thr Arg Ile Ile Trp Glu Leu Ile Lys Glu Lys Leu
44 15 20 25 30
46 att ttt ccc tac gtg gaa ttg gat cta cat agc tat gat tta ggc ata      384
47 Ile Phe Pro Tyr Val Glu Leu Asp Leu His Ser Tyr Asp Leu Gly Ile
48 35 40 45
50 gag aat cgt gat gcc acc aac gac caa gtc acc aag gat gct gca gaa      432
51 Glu Asn Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu
52 50 55 60
54 gct ata aag aag cat aat gtt ggc gtc aaa tgt gcc act atc act cct      480
55 Ala Ile Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro
56 65 70 75
58 gat gag aag agg gtt gag gag ttc aag ttg aaa caa atg tgg aaa tca      528
59 Asp Glu Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser
60 80 85 90
62 cca aat ggc acc ata cga aat att ctg ggt ggc acg gtc ttc aga gaa      576
63 Pro Asn Gly Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu
64 95 100 105 110
67 gcc att atc tgc aaa aat atc ccc cgg ctt gtg agt gga tgg gta aaa      624

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68 Ala Ile Ile Cys Lys Asn Ile Pro Arg Leu Val Ser Gly Trp Val Lys
69          115          120          125
71 cct atc atc ata ggt cgt cat gct tat ggg gat caa tac aga gca act      672
72 Pro Ile Ile Ile Gly Arg His Ala Tyr Gly Asp Gln Tyr Arg Ala Thr
73          130          135          140
75 gat ttt gtt gtt cct ggg cct gga aaa gta gag ata acc tac aca cca      720
76 Asp Phe Val Val Pro Gly Pro Gly Lys Val Glu Ile Thr Tyr Thr Pro
77          145          150          155
79 agt gac gga acc caa aag gtg aca tac ctg gta cat aac ttt gaa gaa      768
80 Ser Asp Gly Thr Gln Lys Val Thr Tyr Leu Val His Asn Phe Glu Glu
81          160          165          170
83 ggt ggt ggt gtt gcc atg ggg atg tat aat caa gat aag tca att gaa      816
84 Gly Gly Gly Val Ala Met Gly Met Tyr Asn Gln Asp Lys Ser Ile Glu
85 175          180          185          190
87 gat ttt gca cac agt tcc ttc caa atg gct ctg tct aag ggt tgg cct      864
88 Asp Phe Ala His Ser Ser Phe Gln Met Ala Leu Ser Lys Gly Trp Pro
89          195          200          205
91 ttg tat ctg agc acc aaa aac act att ctg aag aaa tat gat ggg cgt      912
92 Leu Tyr Leu Ser Thr Lys Asn Thr Ile Leu Lys Lys Tyr Asp Gly Arg
93          210          215          220
95 ttt aaa gac atc ttt cag gag ata tat gac aag cag tac aag tcc cag      960
96 Phe Lys Asp Ile Phe Gln Glu Ile Tyr Asp Lys Gln Tyr Lys Ser Gln
97          225          230          235
99 ttt gaa gct caa aag atc tgg tat gag cat agg ctc atc gac gac atg      1008
100 Phe Glu Ala Gln Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met
101          240          245          250
103 gtg gcc caa gct atg aaa tca gag gga ggc ttc atc tgg gcc tgt aaa      1056
104 Val Ala Gln Ala Met Lys Ser Glu Gly Gly Phe Ile Trp Ala Cys Lys
105 255          260          265          270
107 aac tat gat ggt gac gtg cag tct gac tct gtg gcc caa ggg tat ggc      1104
108 Asn Tyr Asp Gly Asp Val Gln Ser Asp Ser Val Ala Gln Gly Tyr Gly
109          275          280          285
111 tct ctc ggc atg atg acc agc gtg ctg gtt tgt cca gat ggc aag aca      1152
112 Ser Leu Gly Met Met Thr Ser Val Leu Val Cys Pro Asp Gly Lys Thr
113          290          295          300
115 gta gaa gca gag gct gcc cac ggg act gta acc cgt cac tac cgc atg      1200
116 Val Glu Ala Glu Ala Ala His Gly Thr Val Thr Arg His Tyr Arg Met
117          305          310          315
119 tac cag aaa gga cag gag acg tcc acc aat ccc att gct tcc att ttt      1248
120 Tyr Gln Lys Gly Gln Glu Thr Ser Thr Asn Pro Ile Ala Ser Ile Phe
121          320          325          330
123 gcc tgg acc aga ggg tta gcc cac aga gca aag ctt gat aac aat aaa      1296
124 Ala Trp Thr Arg Gly Leu Ala His Arg Ala Lys Leu Asp Asn Asn Lys
125 335          340          345          350
127 gag ctt gcc ttc ttt gca aat gct ttg gaa gaa gtc tct att gag aca      1344
128 Glu Leu Ala Phe Phe Ala Asn Ala Leu Glu Glu Val Ser Ile Glu Thr
129          355          360          365
131 att gag gct ggc ttc atg acc aag gac ttg gct gct tgc att aaa ggt      1392
132 Ile Glu Ala Gly Phe Met Thr Lys Asp Leu Ala Ala Cys Ile Lys Gly

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133          370          375          380
135 tta ccc aat gtg caa cgt tct gac tac ttg aat aca ttt gag ttc atg      1440
136 Leu Pro Asn Val Gln Arg Ser Asp Tyr Leu Asn Thr Phe Glu Phe Met
137          385          390          395
139 gat aaa ctt gga gaa aac ttg aag atc aaa cta gct cag gcc aaa ctt      1488
140 Asp Lys Leu Gly Glu Asn Leu Lys Ile Lys Leu Ala Gln Ala Lys Leu
141          400          405          410
143 taa gttcatacct gagctaagaa ggataattgt cttttggttaa ctaggtctac      1541
145 aggtttacat ttttctgtgt tacactcaag gataaaggca aaatcaattt tgtaatttgt      1601
147 ttagaagcca gagtttatct tttctataag tttacagcct ttttcttata tatacagtta      1661
149 ttgccacctt tgtgaacatg gcaagggact tttttacaat ttttatttta ttttctagta      1721
151 ccagcctagg aattcgggta gtactcattt gtattcactg tcactttttc tcatgttcta      1781
153 attataaatg accaaaatca agattgctca aaagggtaaa tgatagccac agtattgctc      1841
155 cctaaaatat gcataaagta gaaattcact gccttcccct cctgtccatg accttgggca      1901
157 caggggaagt ctggtgtcat agatatcccg ttttgtgagg tagagctgtg cattaaactt      1961
159 gcacatgact ggaacgaagt aggagtgcaa ctcaaagtgt ttgaagatac tgcagtcatt      2021
161 tttgtaaaga ccttgctgaa tgtttccaat agactaaata ctgtttaggc cgcaggagag      2081
163 tttggaatcc ggaataaata ctacctggag gtttgtcctc tccatttttc tctttctcct      2141
165 cctggcctgg cctgaatatt atactactct aaatagcata tttcatccaa gtgcaataat      2201
167 gtaagctgaa tcttttttgg acttctgctg gcctgtttta tttcttttat ataaatgtga      2261
169 tttctcagaa attgatatta aacactatct tatcttctcc      2301
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173 <211> LENGTH: 414
174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapiens
177 <400> SEQUENCE: 2
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180 1          5          10          15
183 Glu Met Thr Arg Ile Ile Trp Glu Leu Ile Lys Glu Lys Leu Ile Phe
184          20          25          30
187 Pro Tyr Val Glu Leu Asp Leu His Ser Tyr Asp Leu Gly Ile Glu Asn
188          35          40          45
191 Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu Ala Ile
192          50          55          60
195 Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro Asp Glu
196 65          70          75          80
199 Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser Pro Asn
200          85          90          95
203 Gly Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu Ala Ile
204          100          105          110
207 Ile Cys Lys Asn Ile Pro Arg Leu Val Ser Gly Trp Val Lys Pro Ile
208          115          120          125
211 Ile Ile Gly Arg His Ala Tyr Gly Asp Gln Tyr Arg Ala Thr Asp Phe
212          130          135          140
215 Val Val Pro Gly Pro Gly Lys Val Glu Ile Thr Tyr Thr Pro Ser Asp
216 145          150          155          160
219 Gly Thr Gln Lys Val Thr Tyr Leu Val His Asn Phe Glu Glu Gly Gly
220          165          170          175
223 Gly Val Ala Met Gly Met Tyr Asn Gln Asp Lys Ser Ile Glu Asp Phe

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224          180          185          190
227 Ala His Ser Ser Phe Gln Met Ala Leu Ser Lys Gly Trp Pro Leu Tyr
228          195          200          205
231 Leu Ser Thr Lys Asn Thr Ile Leu Lys Lys Tyr Asp Gly Arg Phe Lys
232          210          215          220
235 Asp Ile Phe Gln Glu Ile Tyr Asp Lys Gln Tyr Lys Ser Gln Phe Glu
236 225          230          235          240
239 Ala Gln Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met Val Ala
240          245          250          255
243 Gln Ala Met Lys Ser Glu Gly Gly Phe Ile Trp Ala Cys Lys Asn Tyr
244          260          265          270
247 Asp Gly Asp Val Gln Ser Asp Ser Val Ala Gln Gly Tyr Gly Ser Leu
248          275          280          285
251 Gly Met Met Thr Ser Val Leu Val Cys Pro Asp Gly Lys Thr Val Glu
252          290          295          300
255 Ala Glu Ala Ala His Gly Thr Val Thr Arg His Tyr Arg Met Tyr Gln
256 305          310          315          320
259 Lys Gly Gln Glu Thr Ser Thr Asn Pro Ile Ala Ser Ile Phe Ala Trp
260          325          330          335
263 Thr Arg Gly Leu Ala His Arg Ala Lys Leu Asp Asn Asn Lys Glu Leu
264          340          345          350
267 Ala Phe Phe Ala Asn Ala Leu Glu Glu Val Ser Ile Glu Thr Ile Glu
268          355          360          365
271 Ala Gly Phe Met Thr Lys Asp Leu Ala Ala Cys Ile Lys Gly Leu Pro
272          370          375          380
275 Asn Val Gln Arg Ser Asp Tyr Leu Asn Thr Phe Glu Phe Met Asp Lys
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283 <210> SEQ ID NO: 3
284 <211> LENGTH: 1740
285 <212> TYPE: DNA
286 <213> ORGANISM: Homo sapiens
289 <220> FEATURE:
290 <221> NAME/KEY: CDS
291 <222> LOCATION: (87)..(1445)
293 <400> SEQUENCE: 3
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297 Met Ala Gly Tyr Leu Arg Val Val Arg
298          1          5
300 tcg ctc tgc aga gcc tca ggc tcg cgg ccg gcc tgg gcg ccg gcg gcc 161
301 Ser Leu Cys Arg Ala Ser Gly Ser Arg Pro Ala Trp Ala Pro Ala Ala
302 10          15          20          25
304 ctg aca gcc ccc acc tcg caa gag cag ccg cgg cgc cac tat gcc gac 209
305 Leu Thr Ala Pro Thr Ser Gln Glu Gln Pro Arg Arg His Tyr Ala Asp
306          30          35          40
308 aaa agg atc aag gtg gcg aag ccc gtg gtg gag atg gat ggt gat gag 257
309 Lys Arg Ile Lys Val Ala Lys Pro Val Val Glu Met Asp Gly Asp Glu

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310		45		50		55		
312	atg acc cgt att atc tgg cag ttc atc aag gag aag ctc atc ctg ccc							305
313	Met Thr Arg Ile Ile Trp Gln Phe Ile Lys Glu Lys Leu Ile Leu Pro							
314		60		65		70		
316	cac gtg gac atc cag cta aag tat ttt gac ctc ggg ctc cca aac cgt							353
317	His Val Asp Ile Gln Leu Lys Tyr Phe Asp Leu Gly Leu Pro Asn Arg							
318		75		80		85		
322	gac cag act gat gac cag gtc acc att gac tct gca ctg gcc acc cag							401
323	Asp Gln Thr Asp Asp Gln Val Thr Ile Asp Ser Ala Leu Ala Thr Gln							
324	90		95		100		105	
326	aag tac agt gtg gct gtc aag tgt gcc acc atc acc cct gat gag gcc							449
327	Lys Tyr Ser Val Ala Val Lys Cys Ala Thr Ile Thr Pro Asp Glu Ala							
328		110		115		120		
330	cgt gtg gaa gag ttc aag ctg aag aag atg tgg aaa agt ccc aat gga							497
331	Arg Val Glu Glu Phe Lys Leu Lys Lys Met Trp Lys Ser Pro Asn Gly							
332		125		130		135		
334	act atc cgg aac atc ctg ggg ggg act gtc ttc cgg gag ccc atc atc							545
335	Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu Pro Ile Ile							
336		140		145		150		
338	tgc aaa aac atc cca cgc cta gtc cct ggc tgg acc aag ccc atc acc							593
339	Cys Lys Asn Ile Pro Arg Leu Val Pro Gly Trp Thr Lys Pro Ile Thr							
340		155		160		165		
342	att ggc agg cac gcc cat ggc gac cag tac aag gcc aca gac ttt gtg							641
343	Ile Gly Arg His Ala His Gly Asp Gln Tyr Lys Ala Thr Asp Phe Val							
344	170		175		180		185	
346	gca gac cgg gcc ggc act ttc aaa atg gtc ttc acc cca aaa gat ggc							689
347	Ala Asp Arg Ala Gly Thr Phe Lys Met Val Phe Thr Pro Lys Asp Gly							
348		190		195		200		
350	agt ggt gtc aag gag tgg gaa gtg tac aac ttc ccc gca ggc ggc gtg							737
351	Ser Gly Val Lys Glu Trp Glu Val Tyr Asn Phe Pro Ala Gly Gly Val							
352		205		210		215		
354	ggc atg ggc atg tac aac acc gac gag tcc atc tca ggt ttt gcg cac							785
355	Gly Met Gly Met Tyr Asn Thr Asp Glu Ser Ile Ser Gly Phe Ala His							
356		220		225		230		
358	agc tgc ttc cag tat gcc atc cag aag aaa tgg ccg ctg tac atg agc							833
359	Ser Cys Phe Gln Tyr Ala Ile Gln Lys Lys Trp Pro Leu Tyr Met Ser							
360		235		240		245		
362	acc aag aac acc ata ctg aaa gcc tac gat ggg cgt ttc aag gac atc							881
363	Thr Lys Asn Thr Ile Leu Lys Ala Tyr Asp Gly Arg Phe Lys Asp Ile							
364	250		255		260		265	
366	ttc cag gag atc ttt gac aag cac tat aag acc gac ttc gac aag aat							929
367	Phe Gln Glu Ile Phe Asp Lys His Tyr Lys Thr Asp Phe Asp Lys Asn							
368		270		275		280		
370	aag atc tgg tat gag cac cgg ctc att gat gac atg gtg gct cag gtc							977
371	Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met Val Ala Gln Val							
372		285		290		295		
374	ctc aag tct tcg ggt ggc ttt gtg tgg gcc tgc aag aac tat gac gga							1025
375	Leu Lys Ser Ser Gly Gly Phe Val Trp Ala Cys Lys Asn Tyr Asp Gly							
376		300		305		310		

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/618,143A

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Input Set : A:\078-us1.ST25.txt

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date